Remarks

Claims 1-33 have been withdrawn from consideration for this application. Claims 34-42 remain in consideration for this application with claims 34 and 37 being in independent form. Claims 41 and 42 are new and depend from claims 34 and 37, respectively.

Claims 34-40 were rejected under 35 U.S.C. 112, second paragraph, as being indefinite for "failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention." Claim 34 has been amended to more clearly describe the qualifying conditions in the present invention. The language has been altered to read "A method of screening an individual for cytogenetic abnormalities, said individual having a condition selected from the group consisting of idiopathic mental retardation, mental retardation and at least one other clinical abnormality, mental retardation and cancer, and combinations thereof. . ." Claims 34 and 37 have been amended by deleting "about" from the claim language such that the probes have a length of less than 25 kb. Applicants respectively assert that these amendments overcome the rejections under 35 U.S.C. 112.

Regarding the rejection of claim 36 under 35 U.S.C. 112, using the term "paralogous genes," Applicants respectfully assert that it is possible for two sequences having different chromosomal locations to result in a single detectable hybridization signal. This occurs when the two sequences are near each other on the chromosome. The Action included a definition of paralogous genes as, "two genes or clusters of genes at different chromosomal locations in the same organism that have structural similarities indicating that they derived from a common ancestral gene and have since diverged from the parent copy by mutation and selection or drift." Applicants agree that this is an accurate definition. However, Applicants further note that when these paralogous genes diverge, it is possible that they do not diverge very far in terms of genomic distance. Thus, the signals from the two genes merge and appear to be a single signal. Therefore, it is very possible to have two

different chromosomal locations that are so near each other that they result in what is detected as a single hybridization signal. Accordingly, Applicants assert that this explanation overcomes the rejection.

Claims 34-37 were rejected under 35 U.S.C. 102(b) as being anticipated by Rogan, et. al. Applicant respectfully asserts that one difference in the present invention, compared to the cited reference, is that the sequence and location of the less than 25kb probes are known. Any hybridization signal, therefore, has a much more specific location. Advantageously, such a result is more precise and accurate than was possible using the cited prior art. Using methods of the present invention, those skilled in the art would know the precise sequence and location the probe hybridizes to, thus providing a clear result when a hybridization signal is found. In this cited reference, as well as the other references cited in the other rejections, once the starting sequence is nick translated, the resulting probes are of unknown size and sequence. The probes in the references therefore are detecting sequences within particular chromosomes, but the precise sequences and location to which the probes hybridize to are unknown. In view of the arguments above, Applicants respectfully assert that the rejection has been overcome.

Claims 34-40 were rejected under 35 U.S.C. 102(b) as being anticipated by Flint, et. al. The Examiner stated that Flint teaches hybridization to the 13q arm, however, much like the nick translated probes used in the previous reference, the probe that hybridizes is of unknown sequence and location. Therefore, it is unknown where exactly the probe hybridizes in Flint's study, other than the expanse of the 13q arm. Furthermore, any hybridization signal obtained by probes in the cited references will only be as precise, as to sequence and location, as the starting material prior to nick translation. In other words, if the starting material is 100kb in length, the results cannot be more specific as to location of the hybridization and sequence of the probe than stating that the

hybridization occurred withing that 100kb region. Using the probes of the present invention, of known sequence and location, it is possible to obtain the precise sequence and location of the cytogenetic abnormality on the chromosome. The Examiner also states that "Flint thus teaches a single hybridization signal from a plurality of probes to a single chromosome". Applicants note that the precise location of such a signal as well as the precise sequence of the probes providing such a signal are not known. In contrast, Applicant's probes have the ability to obtain a single hybridization signal from a plurality of probes to a known single sequence and known location. Thus, the probes of the present invention obtain a much more specific result. In view of the arguments above, Applicants respectfully assert that the rejection has been overcome.

Claims 34-40 were rejected under 35 U.S.C. 102(b) as being anticipated by Bentz et. al. Applicants respectfully assert that, as in the two references discussed above, the probes in Bentz are of unknown size and sequence after nick translation. Bentz begins with YAC-probes, which are usually around 215 kb, prior to nick translation. Thus, the specificity of Bentz's probes are limited to the sequence and location spanning the entire length of the 215 kb YAC-probe starting material. In contrast, the probes of the present invention provide specificity as to sequence and location of the individual hybridized probe. The probes in Bentz are therefore limited to detection of hybrdization to a particular chromosome or chromosome arm, whereas the probes of the present invention are sequence and location specific within that arm. Using the probes of the present invention, it is possible to gain a more specific understanding of the sequence and location of cytogenetic abnormalities. In view of the arguments above, Applicants respectfully assert that the rejection has been overcome.

Claims 34-36 were rejected on the ground of nonstatutory obviousness-type double patenting as being unpatentable over claims 1 and 3 of U.S. Patent No. 7,014,997. Applicants respectfully

assert that the probes in the cited reference are directed towards determining the existence of a pathological condition or disease predisposition in an individual or their offspring. The method of 7,014,997 does not indicate the types of conditions, clinical abnormalities, and the like, that potential patients must possess, other than a pathological condition or disease predisposition. In contrast, the probes of the present invention are directed towards patients who have a cytogenetic abnormality selected from the group consisting of ideopathic mental retardation, mental retardation and at least one other clinical abnormality, mental retardation and cancer, and combinations thereof. This language is reflected in the amendment to claim 34. In view of the amendment and the arguments presented, Applicants respectfully assert that this rejection has been overcome.

Claims 37 and 39-40 were rejected on the ground of nonstatutory obviousness-type double patenting as being unpatentable over claims 1 and 3 of U.S. Patent No. 7,014,997. Applicant respectfully asserts that the probes in U.S. Patent No. 7,014,997 are directed towards different regions of the chromosome than those of the current invention. The probes of the current invention are directed towards delineating the extent of a chromosome imbalance in the subtelomeric region. This is reflected in the amendment to claim 37 incorporating this language. U.S. Patent No. 7,014,997 does not teach or suggest probes that hybridize to the subtelomeric region of the chromosome, therefore, applicants assert that this rejection has been overcome.

Claim 38 was rejected on the ground of nonstatutory obviousness-type double patenting as being unpatentable over claim 1 of U.S. Patent No. 7,014,997 in view of Bentz et. al. As stated above, U.S. Patent No. 7,014,997 does not teach or suggest probes that hybridize in the subtelomeric region of the chromosome. In contrast, the probes in the present invention are directed towards the subtelomeric region. This is reflected in the amendment to claim 37 incorporating that language. The probes in Bentz are directed towards determining BCR-ABL fusion in interphase nuclei of

clinical samples to diagnose patients with one of two types of cancers. There is no motivation to combine the references cited above to incorporate the probes used in U.S. Patent No. 7,014,997 to delineate the extent of a chromosome imbalance in patients with ideopathic mental retardation or cancer, as in the present invention. Applicants respectfully assert that the amendments to the claims, as well as the arguments presented above, transverse the nonstatutory obviousness-type double patenting rejection of claim 38.

In view of the foregoing, it is respectfully submitted that all rejections have been overcome and that the claims as they now stand are patentable over the art of record and a Notice of Allowance appears to be in order.

Respectfully Submitted,

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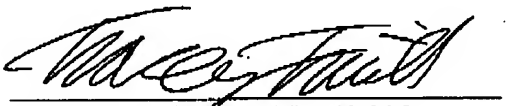
By: 

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(Docket No. 33026)